

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 15, 2001, 10:52:55 ; Search time 30.06 Seconds
(without alignments)
31.624 Million cell updates/sec

Title: US-09-288-719-2

Perfect score: 75

Sequence: 1 GGGSGGGRASGGGS 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 segs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

PIR_66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	94.7	233	2	JC5322
2	65	86.7	643	1	KRH02
3	62	82.7	206	2	I53066
4	61	81.3	102	2	D71415
5	60	80.0	401	1	OZ20AC
6	60	80.0	465	2	G02738
7	60	80.0	592	2	E82759
8	60	80.0	779	2	A35006
9	60	80.0	1433	2	A46053
10	60	80.0	1585	2	T31611
11	59	78.7	136	2	T29282
12	59	78.7	221	2	T04592
13	59	78.7	291	1	S31415
14	59	78.7	316	2	T20497
15	59	78.7	558	2	A33616
16	59	78.7	561	2	A31994
17	58	78.7	593	1	KRH00
18	58	77.3	214	1	KNN72S
19	58	77.3	268	2	A56446
20	58	77.3	284	2	S74256
21	58	77.3	330	2	A39065
22	58	77.3	333	2	A39065
23	58	77.3	427	2	A33272
24	58	77.3	435	2	T15143
25	58	77.3	481	2	A35628
26	58	77.3	495	2	B71360
27	58	77.3	549	2	B32372
28	58	77.3	877	2	T43449
29	57	76.0	239	2	S49193

30	57	76.0	265	2	A40649	hypothetical prote
31	57	76.0	266	1	CIRBL	calpain (EC 3.4.22
32	57	76.0	268	2	S09860	hypothetical prote
33	57	76.0	271	2	S34666	glycine-rich prote
34	57	76.0	312	2	T25048	hypothetical prote
35	57	76.0	396	2	T49109	glycine-rich prote
36	57	76.0	431	1	WJHU2G	homeotic protein H
37	57	76.0	500	2	T22068	hypothetical prote
38	57	76.0	525	1	S11485	hypothetical prote
39	57	76.0	586	2	T26667	RNA helicase - fru
40	57	76.0	1454	2	T13709	hypothetical prote
41	57	76.0	80	2	T10550	diacylglycerol kin
42	56	74.7	157	1	S14857	hypothetical prote
43	56	74.7	157	2	S04536	glycine-rich prote
44	56	74.7	157	2	S04536	embryonic abundant
45	56	74.7	165	1	KNR2G1	glycine-rich cell

ALIGNMENTS

RESULT 1
JC5322
p53 specific single-chain antibody Pab421 - human
C:Species: Homo sapiens (man)
C:Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
C:Accession: JC5322
R:Jannot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A:Title: Characterization of scFv-421, a single-chain antibody targeted to p53.
A:Reference number: JC5322; MUID:97168950
A:Accession: JC5322
A:Molecule type: mRNA
A:Residues: 1-233 <JAN>
A:Experimental source: hydrioloma cell
C:Comment: This protein specifically binds the tumor suppressor protein p53. It resto

Query Match 94.7%; Score 71; DB 2; Length 233;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGSGGGRASGGC 13
DB 110 GGGSGGGRASGGC 122

RESULT 2

KRH02
keratin I, type II, cytoskeletal - human
N:Alternate names: 67K type II epidermal keratin; cytokeratin 1
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 22-Oct-1999 #text_change 10-Dec-1999
C:Accession: A22940; A02950; A43342
R:Johnson, L.D.; Idler, W.W.; Zhou, X.M.; Roop, D.R.; Steinert, P.M.
Proc. Natl. Acad. Sci. U.S.A. 82, 1896-1900, 1985
A:Reference number: A22940; MUID:85166239
A:Accession: A22940
A:Molecule type: DNA
A:Residues: 1-643 <JOH>
A:Cross-references: GB:M98776; GB:M11215; GB:M11845; GB:M11846; NID:g1843461
A:Note: translation of Initiator Met is not shown
R:Steinert, P.M.; Parry, D.A.D.; Idler, W.W.; Johnson, L.D.; Steven, A.C.; Roop, D.R.
J. Biol. Chem. 260, 7142-7149, 1985
A:Title: Amino acid sequences of mouse and human epidermal type II keratins of M-r 67
kDa filament subunits.
A:Reference number: A92535; MUID:85207740
A:Accession: A02950
A:Molecule type: mRNA
A:Residues: 151-183, 'K', 185-199, 'M', 201-204, 'K', 206-236, 'S', 238-239, 'R', 241-356, 'Y', 3
'S', 658-643 <STE>
A:Cross-references: GB:M10938; NID:g186787; PIDN:AAA36153.1; PID:g386854
A:Experimental source: tissue neonatal foreskin

A:Note: the authors translated the codon CUG for residue 476 as Met
R:Chipev, C.C.; Korge, B.P.; Markova, N.; Bale, S.J.; Digiovanna, J.J.; Compton, J.G.;
Cell 70, 821-828, 1992
A:Title: A leucine----proline mutation in the H1 subdomain of keratin 1 causes epidermol
A:Reference number: A43342; MUID:92386601

A:Accession: A43342

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 144-146, 'P', 148-159, 'P', 161-183, 'K', 185-186 <CHI>

A:Cross-references: GB:M68776; GB:M11215; GB:M1845; GB:M1846; NID:g1843461

A:Note: sequence extracted from NCBI backbone (NCBI:112784)

C:Comment: The cytoskeletal and microfilament keratins are classified into two types, t
atin IF protein subunit appears to be a heterotrimer of two type I and two type II pro
C:Comment: Keratin 1 is expressed in terminally differentiating epidermis.

C:Genetics:

A:Gene: GDB:KR11

A:Cross-references: GDB:128198; OMIM:139350

A:Map position: 12q11-12q13

A:Note: defects in this gene may result in epidermolytic hyperkeratosis

C:Complex: heterotrimer of two type I, usually keratin 10 (see PIR:KRHU0), and two tyh

C:Superfamily: cytoskeletal keratin

C:Keywords: coiled coil; heterotrimer; intermediate filament

F:4-179/Domain: head <HEAD>

F:4-143/Region: E1 and V1 subdomains

F:14-179/Region: H1 subdomain

F:180-492/Domain: rod <ROD>

F:180-214/Region: coil 1A

F:215-226/Region: linker 1

F:227-327/Region: coil 1B

F:328-344/Region: linker 12

F:345-363/Region: coil 2A

F:364-371/Region: linker 2

F:372-492/Region: coil 2B

F:430/Region: stutter

F:493-643/Domain: tail <END>

F:493-512/Region: H2 subdomain

F:513-643/Region: V2 and E2 subdomains

Query Match 86.7%; Score 65; DB 1; Length 643;
Best Local Similarity 85.7%; Pred. No. 1.3;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGSGGGRASGGGS 14
DB 594 GGGSGGGRASGGGS 607

RESULT 3
153066
gene M-twist protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I53066; I66795

R:Wolf, C.; Thisse, C.; Stroetzel, C.; Thisse, B.; Gerlinger, P.; Perrin-Schmitt, F.
Dev. Biol. 143, 363-373, 1991

A:Title: The M-twist gene of Mus is expressed in subsets of mesodermal cells and is clos
A:Reference number: I53066; MUID:91122450

A:Accession: I53066

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-206 <RES>

A:Cross-references: GB:M63649; NID:g202243; PIDN:AAA0514.1; PID:g202244

A:Accession: I66795

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-35, 'R', 37-90, 'P', 92-206 <RE2>
A:Cross-references: GB:M63650; NID:g202245; PIDN:AAA0515.1; PID:g202246
C:Genetics:
A:Gene: M-twist

Query Match 82.7%; Score 62; DB 2; Length 206;

Best Local Similarity 78.6%; Pred. No. 1;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGSGGGRASGGGS 14
DB 90 GGGSGGGRASGGGS 103

RESULT 4

D71415
hypothetical protein - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

A:Variety: Columbia

C:Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 05-Dec-1998

C:Accession: D71415

R:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; D
P.; Medler, H.; Medler, E.; Wandut, R.; Meltzenger, T.; Pohl, T.M.; Terry, N.; G
atnagh, T.; Hempel, S.; Kotter, P.; Ertlan, K.D.; Rieger, M.; Schaeffer, M.; Funk, B
ature 391, 485-488, 1998

A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Pulgdomen
ehoff, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.;
C.; Chalvatris, N.

A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis t

A:Reference number: A71400; MUID:98121113

A:Accession: D71415

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-102 <BEV>

A:Cross-references: GB:Z97338; NID:g2244870; PID:e326910; PID:g2244873

C:Genetics:

A:Map position: 4COP9-4G3845

Query Match 81.3%; Score 61; DB 2; Length 102;
Best Local Similarity 78.6%; Pred. No. 0.73;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGSGGGRASGGGS 14
DB 50 GGGSGGGRASGGGS 63

RESULT 5
OZZOAC
circumsporozoite protein precursor - Plasmodium cynomolgi (strain Gombak)
N:Alternate names: major sporozoite surface antigen
C:Species: Plasmodium cynomolgi
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 07-Nov-1997
C:Accession: E26255

R:Galinski, M.R.; Arnot, D.E.; Cochrane, A.H.; Barnwell, J.W.; Nussenzweig, R.S.; Ene
Cell 48, 311-319, 1987

A:Title: The circumsporozoite gene of the Plasmodium cynomolgi complex.

A:Reference number: A90889; MUID:87102878

A:Accession: E26255

A:Molecule type: DNA

A:Residues: 1-401 <GAL>

C:Comment: There are three distinct regions in the mature circumsporozoite protein, t
obic membrane anchoring sequence.

C:Comment: There are 17 tandem copies of the 11-residue repeat D/G-G-A-A-A-G-G-G-G-
C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology

C:Keywords: sporozoite; surface antigen; tandem repeat

F:1-19/Domain: signal sequence #status predicted <Sig>
F:20-401/Product: circumsporozoite protein #status predicted <MNT>
F:88-278/Region: 11-residue repeats
F:326-379/Domain: thrombospondin type 1 repeat homology <THRL>

Query Match 80.0%; Score 60; DB 1; Length 401;
Best Local Similarity 71.4%; Pred. No. 3.1;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGSGGGRASGGGS 14

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Db      256 GGGGNGGAAGGCG 269

RESULT      6
F82738
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 19-May-2000
C:Accession: G02738
R:Enserback, S.
submitted to the EMBL Data Library, June 1996
A:Reference number: H01646
A:Accession: G02738
A:Status: Preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-465 <ENE>
A:Cross-references: EMBL:U59832; NID:g1399238; PID:g1399239
C:Genetics:
A:Gene: FREAC-4
C:Superfamily: unassigned fork head proteins; fork head DNA-binding domain homology
F:125-216/Domain: fork head DNA-binding domain homology <FHD>

Query Match      80.0%; Score 60; DB 2; Length 465;
Best Local Similarity 78.6%; Pred. NO. 3.5;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GGGGSGGRASGCG 14
      1111111111111111
Db      101 GGGGSGGRASGCG 114

RESULT      7
E82759
endo-1,4-beta-glucanase XF0818 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: E82759
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MIMD:20365717
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: E82759
A:Status: preliminary
A:Molecule type: DNA
A:Cross-references: GB:AE003921; GB:AE003849; NID:g9105710; PIDN:AAF83628.1; GSPDB:GN001
A:Experimental source: strain 9a5c
R:Simpton, A.J.G.; Relnack, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
B:Rios, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carer, H
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincan, A.P.; Ferreira, A.J.S.
submitted to GeneBank, June 2000
A:Authors: Ferreira, V.C.A.; Perro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
I.D.; Junqueira, M.L.; Kemper, E.L.; Kitejima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laiy
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.;
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sasaki
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
M.; Tsunako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF0818

Query Match      80.0%; Score 60; DB 2; Length 592;
Best Local Similarity 84.6%; Pred. NO. 4.4;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GGGGSGGRASGCG 13
      1111111111111111

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RESULT      8
A35006
Cell surface glycoprotein msp130 precursor - sea urchin (Strongylocentrotus purpuratus)
C:Species: Strongylocentrotus purpuratus (purple urchin)
C:Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 09-Sep-1997
C:Accession: A35006; A45939
R:Part, B.A.; Parks, A.L.; Raff, R.A.
J. Biol. Chem. 265, 1408-1413, 1990
A:Title: Promoter structure and protein sequence of msp130, a lipid-anchored sea urchin
A:Reference number: A35006; MUID:90110195
A:Accession: A35006
A:Status: Preliminary
A:Molecule type: DNA; mRNA
A:Residues: 1-779 <PAR>
A:Cross-references: GB:M31751, NID:g161543; PID:g161544; GB:J05204
R:Leff, D.S.; Anstrom, J.A.; Chln, J.E.; Harkey, M.A.; Showman, R.M.; Raff, R.A.
Dev. Biol. 121, 29-40, 1987
A:Title: Antibodies to a fusion protein identify a cDNA clone encoding msp130, a prim
A:Reference number: A45939; MUID:97191419
A:Accession: A45939
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 542-779 <LEA>
A:Cross-references: GB:M16457; NID:g161539; PID:g161540
C:Keywords: glycoprotein

Query Match      80.0%; Score 60; DB 2; Length 779;
Best Local Similarity 76.9%; Pred. No. 5.5;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY      1 GGGGSGGRASGG 13
        |||||111111
DB      57 GGGGSGGRGGGG 69

RESULT      9
A46053
Bullous pemphigoid antigen, BPAG2, type XVII collagen alpha 1-chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Sep-1993 #sequence_revision 21-Sep-1993 #text_change 05-Nov-1999
C:Accession: A46053
R:Li, K.; Tamai, K.; Tan, E.M.L.; Dittto, J.
J. Biol. Chem. 268, 8825-8834, 1993
A:Title: Cloning of type XVII collagen. Complementary and genomic DNA sequences of mo
egment, and unusual features in the 5'-end of the gene and the 3'-untranslated region
A:Reference number: A46053; MUID:93232041
A:Accession: A46053
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-1433 <LIT>
A:Cross-references: GB:L08407; NID:g309182; PID:AAA37443.1; PID:g309183
A:Note: sequence extracted from NCBI backbone (NCBIN:129627, NCBI:P:129628)

Query Match      80.0%; Score 60; DB 2; Length 1433;
Best Local Similarity 84.6%; Pred. No. 9.4;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1 GGGGSGGRASGG 13
        |||||111111
DB      443 GGGGSGGRASGG 455

RESULT      10
T31611
Hypothetical protein Y50E8a.g - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T31611

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R.Steward, C.
 Submitted to the EMBL Data Library, September 1999
 A:Reference number: 221047
 A:Accession: T31611
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1585 <WILL>
 A:Cross-references: EMBL:AL117200; NID:e1549770; PIDN:CAB55050.1; CESP:Y50E8A.g
 C:Genetics:
 A:Experimental source: clone Y50E8A
 A:Gene: CESP:Y50E8A.g
 A:Introns: 25/3; 60/1; 133/2; 217/3; 270/3; 337/2; 400/1; 746/2

Query Match
 Best Local Similarity 84.6%; Pred. No. 10;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGGGSGGRASGGG 13
 DB 452 GGGGSGGRASGGG 464

RESULT 11
 T29282
 hypothetical protein C34D4.11 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
 C:Accession: T29282
 R:Du, Z.; Le, T.T.
 submitted to the EMBL Data Library, May 1996
 A:Description: The sequence of C. elegans cosmid C34D4.
 A:Reference number: 220600
 A:Accession: T29282
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-136 <DUZ>
 A:Cross-references: EMBL:U58755; PIDN:AAB00696.1; GSPDB:GN00022; CESP:C34D4.11
 A:Experimental source: strain Bristol N2; clone C34D4
 C:Genetics:
 A:Gene: CESP:C34D4.11
 A:Map position: 4
 A:Introns: 20/1; 66/1; 98/1; 116/1
 C:Superfamily: Arabidopsis glycine-rich protein 3

Query Match
 Best Local Similarity 78.7%; Score 59; DB 2; Length 136;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GGGGSGGRASGGG 13
 DB 97 GGGGSGGRASGGG 109

RESULT 12
 T04592
 glycine-rich cell wall structural protein homolog F23E13.120 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 14-May-1999
 C:Accession: T04592
 R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Jesse, T.
 submitted to the Protein Sequence Database, March 1998
 A:Reference number: Z15378
 A:Accession: T04592
 A:Molecule type: DNA
 A:Residues: 1-221 <BEV>
 A:Cross-references: EMBL:AL022141
 A:Experimental source: cultivar Columbia; BAC clone F23E13
 C:Genetics:
 A:Map position: 4
 A:Note: F23E13.120

Query Match
 Best Local Similarity 78.7%; Score 59; DB 2; Length 221;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGGGSGGRASGGG 13
 DB 98 GGGGSGGRASGGG 110

RESULT 13
 S31415
 glycine-rich protein GRP22 - rape
 C:Species: Brassica napus (rape)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: S31415
 R:Bergeron, D.; Boivin, R.; Baszczyński, C.L.; Bellemare, G.
 submitted to the EMBL Data Library, August 1992
 A:Description: Characterization and expression of a gene family encoding glycine-rich
 A:Reference number: S31415
 A:Accession: S31415
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-291 <BER>
 A:Cross-references: EMBL:Z15045; NID:g17820; PIDN:CAA78762.1; PID:g17821
 C:Superfamily: Phaseolus glycine-rich cell wall protein 1.8

Query Match
 Best Local Similarity 78.7%; Score 59; DB 1; Length 291;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 GGGGSGGRASGGG 14
 DB 115 GGGGSGGRASGGG 128

RESULT 14
 T20497
 hypothetical protein F02D10.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T20497
 R:Swingburne, J.
 submitted to the EMBL Data Library, November 1995
 A:Reference number: Z19283
 A:Accession: T20497
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-316 <WILL>
 A:Cross-references: EMBL:Z67990; PIDN:CAA91932.1; GSPDB:GN00028; CESP:F02D10.1
 A:Experimental source: clone F02D10
 C:Genetics:
 A:Gene: CESP:F02D10.1
 A:Map position: X
 A:Introns: 56/3
 C:Superfamily: unassigned collagens

Query Match
 Best Local Similarity 78.7%; Score 59; DB 2; Length 316;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGGGSGGRASGGG 13
 DB 98 GGGGSGGRASGGG 110

RESULT 15
 A33616
 heterogeneous ribonuclear particle protein L - human
 C:Species: Homo sapiens (man)
 C:Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 15-Sep-2000

C:Accession: A33616
R:PIN1-Roma, S.; Swanson, M.S.; Gall, J.G.; Dreyfuss, G.
J. Cell Biol. 109, 2575-2587, 1989
A:Title: A novel heterogeneous nuclear RNP protein with a unique distribution on nascent
A:Reference number: A33616; MUID:90078296
A:Accession: A33616
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-558 <PIN>
A:Cross-references: GB:X16135; NID:q32355; PIDN:CAA34261.1; PID:q32356
C:Superfamily: Caenorhabditis elegans hypothetical protein C44B7.2

Query Match 78.7%; Score 59; DB 2; Length 558;
Best Local Similarity 78.6%; Pred. No. 5.4;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGSGSGGRASGGGS 14
|||||
DB 8 GGSGSGGRYRGGS 21

Search completed: March 15, 2001, 10:52:56
Job time: 1005 sec